41. An antibody of claim 32.

Amendments to the Specification:

On page 6, after line 2, please **insert** the following paragraphs:

-- The HPT1, hPEPT1, D2H, and hSI receptors were selected for cloning as GIT receptor targets based on several criteria, including: (1) expression on surface of epithelial cells in gastro-intestinal tract (GIT); (2) expression along the length of small intestine (HPT1, hPEPT1, D2H); (3) expression locally at high concentration (hSI); (4) large putative extracellular domains facing into the lumen of the GIT; and (5) extracellular domains that permit easy access and bioadhesion by targeting particles.

The four recombinant receptor sites screened with the peptide libraries additionally have the following characteristics:

Receptor	Characteristics
D2H	Transport of neutral/basic amino acids; a transport activating protein for a range of amino acid translocases
hS1	Metabolism of sucrose and other sugars, represents 9% of brush border membrane protein Jejunum
HPT1	di/tri peptide transporter or facilitator of peptide transport
hPEPT1	di/tri peptide transporter

The following receptor domains were cloned and expressed as His-tag fusion proteins by standard techniques:

Cloning of Extracellular Domain of Selected Receptor Site

Receptor	Domain (amino acid residues)	SEQ ID NOS
hPEPT1[a]	391-571	16
HPT1[b]	29-273	15
hSI[c]	272-667	14

[a] Liang et al., 1995, J. Biol. Chern. 270: 6456-6463;
[b] Dantzig et al., 1994, Association of Intestinal Peptide Transport with a Protein Related to the Cadherin Superfamily;
[c] Chantret et al., Biochem. J. 285: 915-923;
[d] Bertran et al., J. Biol. Chem. 268: 14842-14949.

The receptor proteins were expressed as His-tag fusion proteins and affinity purified under denaturing conditions, using urea or guanidine HCl, utilizing the pET His-tag metal chelate affinity for Ni-NTA Agarose (Hochuli, E., Purification of recombinant proteins with metal chelate adsorbent, Genetic Engineering, Principals and Methods (J.K. Setlow, ed.), Plenum Press, NY, Vol. 12 (1990), pp. 87-98).

As indicated in WO 98/51325, phage which showed specificity to a GIT receptor was further characterized by ELISA on a variety of recombinant proteins. Phage which continued to exhibit GIT receptor specificity was sequenced. Their insert sequences are summarized as follows:

hSI	SEQ. ID.NO	TARGET BINDING PHAGE INSERT SEQUENCE
S15	17.	RSGAYESPDGRGGRSYVGGGGGCGNIGRKHNLWGLRTASPACWD
S21	18.	SPRSFWPVVSRHESFGISNYLGCGYRTCISGTMTKSSPIYPRHS
S22	19.	SSSSDWGGVPGKVVRERFKGRGCGISITSVLTGKPNPCPEPKAA
Sni10	20.	RVGQCTDSDVRRPWARSCAHQGCGAGTRNSHGCITRPLRQASAH
Sni28	21.	SHSGGMNRAYGDVFRELRDRWNATSHHTRPTPQLPRGPN
Sni34	22.	SPCGGSWGRFMQGGLFGGRTDGCGAHRNRTSASLEPPSSDY
Sni38	23.	RGAADQRRGWSENLGLPRVGWDAIAHNSYTFTSRRPRPP
Sni45	24.	SGGEVSSWGRVNDLCARVSWTGCGTARSARTDNKGFLPKHSSLR
SniAX2	25.	SDSDGDHYGLRGGVRCSLRDRGCGLALSTVHAGPPSFYPKLSSP
SniAX4	26.	RSLGNYGVTGTVDVTVLPMPGHANHLGVSSASSSDPPRR

SniAX6	27.	RTTTAKGCLLGSFGVLSGCSFTPTSPPPHLGYPPHSVN
SniAX8	28.	SPKLSSVGVMTKVTELPTEGPNAISIPISATLGPRNPLR

D2H

DAB3	29.	RWCGAELCNSVTKKFRPGWRDHANPSTHHRTPPPSQSSP
DAB7	30	RWCGADDPCGASRWRGGNSLFGCGLRCSAAQSTPSGRIHSTSTS
DAB10	31.	SKSGEGGDSSRGETGWARVRSHAMTAGRFRWYNQLPSDR
DAB18	32.	RSSANNCEWKSDWMRRACIARYANSSGPARAVDTKAAP
DAB24	33.	SKWSWSSRWGSPQDKVEKTRAGCGGSPSSTNCHPYTFAPPPQAG
DAB30	34.	SGFWEFSRGLWDGENRKSVRSGCGFRGSSAQGPCPVTPATIDKH
DAX15	35.	SESGRCRSVSRWMTTWQTQKGGCGSNVSRGSPLDPSHQTGHATT
DAX23	36.	REWRFAGPPLDLWAGPSLPSFNASSHPRALRTYWSQRPR
DAX24	37.	RMEDIKNSGWRDSCRWGDLRPGCGSRQWYPSNMRSSRDYPAGGH
DAX27	38.	SHPWYRHWNHGDFSGSGQSRHTPPESPHPGRPNATI
DCX8	39.	RYKHDIGCDAGVDKKSSSVRGGCGAHSSPPRAGRGPRGTMVSRL
DCX11	40.	SQGSKQCMQYRTGRLTVGSEYGCGMNPARHATPAYPARLLPRYR
DCX26	41.	SGRTTSEISGLWGWGDDRS GYGWGNTLRPNYIPYRQATNRHRYT
DCX33	42.	RWNWTVLPATGGHYWTRSTDYHAINNHRPSIPHQHPTPI
DCX36	43.	SWSSWNWSSKTTRLGDRATREGCGPSQSDGCPYNGRLTTVKPRT
DCX39	44.	SGSLNAWQPRSWVGGAFRSHANNNLNPKPTMVTRHPT
DCX42	45.	RYSGLSPRDNGPACSQEATLEGCGAQRLMSTRRKGRNSRPGWTL
DCX45	46.	SVGNDKTSRPVSFYGRVSDLWNASLMPKRTPSSKRHDDG

hPEPT1

PAX9	47.	RWPSVGYKGNGSDTIDVHSNDASTKRSLIYNHRRPLFP

PAX14	48.	RTFENDGLGVGRSIQKKSDRWYASHNIRSHFASMSPAGK
PAX15	49.	SYCRVKGGGEGGHTDSNLARSGCGKVARTSRLQHINPRATPPSR
PAX16	50.	SWTRWGKHTHGGFVNKSPPGKNATSPYTDAQLPSDQGPP
PAX17	51.	SQVDSFRNSFRWYEPSRALCHGCGKRDTSTTRIHNSPSDSYPTR
PAX18	52.	SFLRFQSPRFEDYSRTISRLRNATNPSNVSDAHNNRALA
PAX35	53.	RSITDGGINEVDLSSVSNVLENANSHRAYRKHRPTLKRP
PAX38	54.	SSKVSSPRDPTVPRKGGNVDYGCGHRSSARMPTSALSSITKCYT
PAX40	55.	RASTQGGRGVAPEFGASVLGRGCGSATYYTNSTSCKDAMGHNYS
PAX43	56.	RWCEKHKFTAARCSAGAGFERDASRPPQPAHRDNTNRNA
PAX45	57.	SFQVYPDHGLERHALDGTGPLYAMPGRWIRARPQNRDRQ
PAX46	58.	SRCTDNEQCPDTGTRSRSVSNARYFSSRLLKTHAPHRP
P31	59.	SARDSGPAEDGSRAVRLNGVENANTRKSSRSNPRGRRHP
P90	60.	SSADAEKCAGSLLWWGRQNNSGCGSPTKKHLKHRNRSQTSSSSH
5PAX3	61.	RPKNVADAYSSQDGAAAEETSHASNAARKSPKHKPLRRP
5PAX5	62.	RGSTGTAGGERSGVLNLHTRDNASGSGFKPWYPSNRGHK
5PAX7	63.	RWGWERSPSDYDSDMDLGARRYATRTHRAPPRVLKAPLP
5PAX12	64.	RGWKCEGSQAAYGDKDIGRSRGCGSITKNNTNHAHPSHGAVAKI

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HAX9	65.	SREEANWDGYKREMSHRSRFWDATHLSRPRRPANSGDPN
HAX35	66.	EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPRK
HAX40	67	REFAERRLWGCDDLSWRLDAEGCGPTPSNRAVKHRKPRPRSPAL
HAX42	68.	SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRRRPSAIPT
HCA3	69.	RHISEYSFANSHLMGGESKRKGCGINGSFSPTCPRSPTPAFRRT
H40	70.	SRESGMWGSWWRGHRLNSTGGNANMNASLPPDPPVSTP
PAX2	71.	STPPSREAYSRPYSVDSDSDTNAKHSSHNRRLRTRSRPN